



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> YAMAMOTO, Takuo
MARUTA, Kazuhiko
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FUKUDA, Shigeharu
MIYAKE, Toshio

<120> NON-REDUCING SACCHARIDE-FORMING ENZYME,
TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
SACCHARIDES USING THE ENZYMES

<130> YAMAMOTO=16A

<140> 09/435,770

<141> 1999-11-08

<150> JP 258,394/1998

<151> 1998-09-11

<150> JP 352,252/1998

<151> 1998-12-11

<150> JP 16,931/1999

<151> 1999-01-26

<160> 39

<170> PatentIn Ver. 2.1

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Glu Gly Leu Ala Glu Leu Ser Arg Ala Ala His Glu Arg Gly Met Gly
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Arg Leu Pro Val Leu Gly Asp Gly Pro Asp Glu Leu Asp Ala Leu Arg
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 Tyr Glu Leu Met Ser Trp Arg Arg Ala Asp His Asp Leu Asn Tyr Arg
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 Arg Val Phe Asp Asp Thr His Arg Glu Ile Gly Arg Trp Ile Ala Glu
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 Ile Trp Val Glu Lys Ile Ile Glu Gly Asp Glu Arg Met Pro Pro Gln
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 Arg Lys Arg Ala Val Ala Arg Gly Ile Leu Asn Ser Glu Ile Arg Arg
 325 330 335
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 Arg Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe
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 Asp Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp
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 Leu Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro
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Leu Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu
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gcc	gcc	gcg	cag	gcc	gca	gcc	ccc	cag	ctc	gag	gcc	gac	ctc	gcc	gcc	1924
Ala	Ala	Ala	Gln	Ala	Ala	Ala	Pro	Gln	Leu	Glu	Ala	Asp	Leu	Ala	Ala	
	380					385					390					
gtc	ggc	gca	gcg	ctc	gcc	gac	ccg	ggc	aac	ccc	gcc	gcg	ctc	cgc	ttc	1972
Val	Gly	Ala	Ala	Leu	Ala	Asp	Pro	Gly	Asn	Pro	Ala	Ala	Leu	Arg	Phe	
395				400						405					410	
cag	cag	acc	agc	ggc	atg	atc	atg	gcc	aag	ggc	gtc	gag	gac	aac	gcg	2020
Gln	Gln	Thr	Ser	Gly	Met	Ile	Met	Ala	Lys	Gly	Val	Glu	Asp	Asn	Ala	
				415					420					425		
ttc	tac	cgc	tac	ccc	cgg	ctc	acc	tcg	ctg	acc	gag	gtc	ggg	gga	gac	2068
Phe	Tyr	Arg	Tyr	Pro	Arg	Leu	Thr	Ser	Leu	Thr	Glu	Val	Gly	Gly	Asp	
			430					435					440			
ccg	agc	ctg	ttc	gcg	atc	gac	gcg	gcc	gcc	ttc	cac	gcg	gcg	cag	cgc	2116
Pro	Ser	Leu	Phe	Ala	Ile	Asp	Ala	Ala	Ala	Phe	His	Ala	Ala	Gln	Arg	
		445					450					455				
gac	cgc	gcc	gcc	cgg	ctg	ccc	gag	tcg	atg	acg	acg	ctg	acc	acc	cac	2164
Asp	Arg	Ala	Ala	Arg	Leu	Pro	Glu	Ser	Met	Thr	Thr	Leu	Thr	Thr	His	
	460					465						470				
gac	acc	aag	cgc	agc	gaa	gac	acc	cgg	gcg	cgg	atc	acc	gcg	ctc	gcc	2212
Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Thr	Ala	Leu	Ala	
475					480					485					490	
gag	gcc	ccc	gaa	cgc	tgg	cgg	cgc	ttc	ctg	acc	gag	gtc	ggc	ggg	ctc	2260
Glu	Ala	Pro	Glu	Arg	Trp	Arg	Arg	Phe	Leu	Thr	Glu	Val	Gly	Gly	Leu	
			495					500						505		
atc	gga	acg	ggc	gac	cgg	gtg	ctg	gag	aac	ctg	atc	tgg	cag	gcg	atc	2308
Ile	Gly	Thr	Gly	Asp	Arg	Val	Leu	Glu	Asn	Leu	Ile	Trp	Gln	Ala	Ile	
			510					515					520			
gtc	ggc	gcg	tgg	ccg	gcg	agc	cgg	gag	cgg	ctc	gag	gcc	tac	gcg	ctg	2356
Val	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Glu	Ala	Tyr	Ala	Leu	
		525					530					535				
aag	gcc	gcg	cgc	gaa	gcc	ggc	gag	tcg	acc	gac	tgg	atc	gac	ggc	gac	2404
Lys	Ala	Ala	Arg	Glu	Ala	Gly	Glu	Ser	Thr	Asp	Trp	Ile	Asp	Gly	Asp	
	540					545					550					
ccc	gcg	ttc	gaa	gag	cgg	ctg	acc	cgc	ctg	gtc	acg	gtc	gcc	gtc	gag	2452
Pro	Ala	Phe	Glu	Glu	Arg	Leu	Thr	Arg	Leu	Val	Thr	Val	Ala	Val	Glu	
555					560					565					570	
gag	ccg	ctc	gtg	cac	gag	ctg	ctc	gag	cgg	ctc	gtc	gac	gag	ctg	acg	2500
Glu	Pro	Leu	Val	His	Glu	Leu	Leu	Glu	Arg	Leu	Val	Asp	Glu	Leu	Thr	
				575					580					585		
gcg	gcc	ggg	tac	tcc	aac	ggc	ctc	gcg	gcg	aag	ctg	ctg	cag	ctg	ctc	2548
Ala	Ala	Gly	Tyr	Ser	Asn	Gly	Leu	Ala	Ala	Lys	Leu	Leu	Gln	Leu	Leu	
			590					595					600			
gcc	ccc	gga	acc	ccc	gac	gtg	tac	cag	ggc	acg	gaa	cgc	tgg	gac	cgg	2596
Ala	Pro	Gly	Thr	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Arg	Trp	Asp	Arg	
		605					610					615				
tcg	ctg	gtg	gac	ccg	gac	aac	cgt	cgc	ccc	gtg	gat	ttc	gcc	gcg	gca	2644
Ser	Leu	Val	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Val	Asp	Phe	Ala	Ala	Ala	
	620					625					630					

tcc gag ctg ctc gac cgc ctc gac ggc ggc tgg cgg ccg ccc gtc gac	2692
Ser Glu Leu Leu Asp Arg Leu Asp Gly Gly Trp Arg Pro Pro Val Asp	
635 640 645 650	
gag acc ggc gcg gtc aag acg ctc gtc gtc tcc cgc gcg ctg cgg ctg	2740
Glu Thr Gly Ala Val Lys Thr Leu Val Val Ser Arg Ala Leu Arg Leu	
655 660 665	
cgc cgc gac cgg ccc gag ctg ttc acc gcg tac cac ccg gtc acg gcg	2788
Arg Arg Asp Arg Pro Glu Leu Phe Thr Ala Tyr His Pro Val Thr Ala	
670 675 680	
cgc ggc gcg cag gcc gag cac ctg atc ggc ttc gac cgc ggc ggc gcg	2836
Arg Gly Ala Gln Ala Glu His Leu Ile Gly Phe Asp Arg Gly Gly Ala	
685 690 695	
atc gcc ctg gcc acc cgc ctg ccg ctc ggc ctc gcc gcc gca ggc ggc	2884
Ile Ala Leu Ala Thr Arg Leu Pro Leu Gly Leu Ala Ala Ala Gly Gly	
700 705 710	
tgg ggc gac acg gtc gtc gac gtc ggc gag cgg agc ctg cgc gac gag	2932
Trp Gly Asp Thr Val Val Asp Val Gly Glu Arg Ser Leu Arg Asp Glu	
715 720 725 730	
ctg acc ggc cgc gag gcc cgc gga gcg gcg cgc gtg gcc gag ttg ttc	2980
Leu Thr Gly Arg Glu Ala Arg Gly Ala Ala Arg Val Ala Glu Leu Phe	
735 740 745	
gcc gac tac ccc gtc gcc ctg ctg gtg gag aca tgaaccgacg attcccggtc	3033
Ala Asp Tyr Pro Val Ala Leu Leu Val Glu Thr	
750 755	
tgggcgcccc aggcgcgcga ggtgacgctc gtcgtgggcc aaggccgcgc cgaactcccg	3093
ctgaccgcgc acgagaacgg atgggtgggct cttcagcagc cgtggggacgg cggccccgac	3153
ctcgtcgact acggctacct cgtcgacggc aagggccctt tcgccgaccc gcggtcgctg	3213
cggcagccgc gcggcgtgca cgagctcggc cgcgaattc	3252

<210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 21
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC

<400> 21
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<210> 22
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 22

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<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 23

gactagtaaa catctagatt cctcctgatt ttattaaaaa ag 42

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 24

aaatctagat gcccgccagt acctaccgcc ttc 33

<210> 25

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 25

aaaactagtt tatcatgtct ccaccagcag ggc 33

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 26

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<210> 27

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

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<210> 28
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC

 <400> 28
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 <210> 29
 <211> 22
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 <220>
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 <400> 29
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 <210> 30
 <211> 22
 <212> DNA
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 <400> 30
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 <210> 31
 <211> 26
 <212> DNA
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 <223> n at position 18 is a, c, g, or t.

 <221> misc_fea
 <222> (18)..(18)

 <400> 31
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 <210> 32
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<222> (477)..(2201)

<220>

<221> 3'UTR

<222> (2202)..(2218)

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gaccgcctcg acggcggctg gcggccgccc gtcgacgaga ccggcgcggt caagacgctc 180
gtcgtctccc gcgcgtcgcg gctgcgccgc gaccggcccc agctgttcac cgcgtaccac 240
ccggtcacgg cgcgcggcgc gcaggccgag cacctgatcg gcttcgaccg cggcggcgcg 300
atcgccctgg ccacccgcct gccgctcggc ctgcgcccg caggcggctg gggcgacacg 360
gtcgtcgacg tcggcgagcg gagcctgcgc gacgagctga ccggccgcga ggcccccgga 420
gcggcgcgcg tggccgagtt gttcgccgac taccctgctg ccctgctggt ggagac atg 479
Met
1

aac cga cga ttc ccg gtc tgg gcg ccc cag gcc gcg cag gtg acg ctc 527
Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr Leu
5 10 15

gtc gtg ggc caa ggc cgc gcc gaa ctc ccg ctg acc cgc gac gag aac 575
Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu Asn
20 25 30

gga tgg tgg gct ctt cag cag ccg tgg gac ggc ggc ccc gac ctc gtc 623
Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu Val
35 40 45

gac tac ggc tac ctc gtc gac ggc aag ggc ccc ttc gcc gac ccg cgg 671
Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro Arg
50 55 60 65

tcg ctg cgg cag ccg cgc ggc gtg cac gag ctc ggc cgc gaa ttc gac 719
Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe Asp
70 75 80

ccc gcc cgc tac gcg tgg ggc gac gac gga tgg cgc ggc cga gac ctc 767
Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp Leu
85 90 95

acc gga gcc gtg atc tac gaa ctg cac gtc ggc acc ttc acc cct gag 815
Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro Glu
100 105 110

gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc 863
Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg Leu
115 120 125

ggc gtc gac gcg gtc gag ctg ctg ccc gtc aac gcg ttc aac ggc acc 911
Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly Thr
130 135 140 145

cac ggc tgg ggc tac gac ggg gtg ctc tgg tac gcg gtg cac gag ccc 959
His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu Pro
150 155 160

tac ggc ggc ccg gag gcg tac cag cgc ttc gtc gac gcc tgc cac gcc 1007

Tyr	Gly	Gly	Pro	Glu	Ala	Tyr	Gln	Arg	Phe	Val	Asp	Ala	Cys	His	Ala		
			165					170					175				
cgc	ggc	ctc	gcc	gtc	gtg	cag	gac	gtc	gtc	tac	aac	cac	ctg	ggc	ccg	1055	
Arg	Gly	Leu	Ala	Val	Val	Gln	Asp	Val	Val	Tyr	Asn	His	Leu	Gly	Pro		
		180					185					190					
agc	ggc	aac	cac	ctg	ccc	gac	ttc	ggc	ccc	tac	ctc	ggg	tcg	ggc	gcc	1103	
Ser	Gly	Asn	His	Leu	Pro	Asp	Phe	Gly	Pro	Tyr	Leu	Gly	Ser	Gly	Ala		
	195					200					205						
gcc	aac	acc	tgg	ggc	gac	gcg	ctg	aac	ctc	gac	ggg	ccg	ctc	tcc	gac	1151	
Ala	Asn	Thr	Trp	Gly	Asp	Ala	Leu	Asn	Leu	Asp	Gly	Pro	Leu	Ser	Asp		
210					215					220					225		
gag	gtg	cgg	cgg	tac	atc	atc	gac	aac	gcg	gtg	tac	tgg	ctg	cgc	gac	1199	
Glu	Val	Arg	Arg	Tyr	Ile	Ile	Asp	Asn	Ala	Val	Tyr	Trp	Leu	Arg	Asp		
				230					235					240			
atg	cac	gcc	gac	ggg	ctg	cgg	ctc	gac	gcc	gtg	cac	gcg	ctg	cgc	gac	1247	
Met	His	Ala	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Val	His	Ala	Leu	Arg	Asp		
			245					250					255				
gcc	cgc	gcg	ctg	cac	ctg	ctc	gaa	gag	ctc	gcc	gcc	cgc	gtc	gac	gag	1295	
Ala	Arg	Ala	Leu	His	Leu	Leu	Glu	Glu	Leu	Ala	Ala	Arg	Val	Asp	Glu		
		260					265					270					
ctg	gcg	ggc	gag	ctc	ggc	cgg	ccg	ctg	acg	ctc	atc	gcc	gag	agc	gac	1343	
Leu	Ala	Gly	Glu	Leu	Gly	Arg	Pro	Leu	Thr	Leu	Ile	Ala	Glu	Ser	Asp		
	275					280					285						
ctg	aac	gac	ccg	aag	ctg	atc	cgc	tcc	cgc	gcg	gcg	cac	ggc	tac	ggc	1391	
Leu	Asn	Asp	Pro	Lys	Leu	Ile	Arg	Ser	Arg	Ala	Ala	His	Gly	Tyr	Gly		
290					295				300					305			
ctc	gac	gcc	cag	tgg	gac	gac	gac	gtg	cac	cac	gcg	gtg	cac	gcc	aac	1439	
Leu	Asp	Ala	Gln	Trp	Asp	Asp	Asp	Val	His	His	Ala	Val	His	Ala	Asn		
				310					315					320			
gtg	acc	ggc	gag	acc	gtc	ggc	tac	tac	gcc	gac	ttc	ggc	ggg	ctc	ggc	1487	
Val	Thr	Gly	Glu	Thr	Val	Gly	Tyr	Tyr	Ala	Asp	Phe	Gly	Gly	Leu	Gly		
			325					330					335				
gcc	ctc	gtc	aag	gtg	ttc	cag	cgc	ggc	tgg	ttc	cac	gac	ggc	acc	tgg	1535	
Ala	Leu	Val	Lys	Val	Phe	Gln	Arg	Gly	Trp	Phe	His	Asp	Gly	Thr	Trp		
		340					345					350					
tcg	agc	ttc	cgc	gag	cgg	cac	cac	ggc	cgg	ccg	ctc	gac	ccc	gac	atc	1583	
Ser	Ser	Phe	Arg	Glu	Arg	His	His	Gly	Arg	Pro	Leu	Asp	Pro	Asp	Ile		
	355					360					365						
ccg	ttc	cgc	cgg	ctc	gtc	gcc	ttc	gcg	cag	gat	cac	gac	cag	gtc	ggc	1631	
Pro	Phe	Arg	Arg	Leu	Val	Ala	Phe	Ala	Gln	Asp	His	Asp	Gln	Val	Gly		
370					375					380					385		
aac	cga	gcg	gtc	ggc	gac	cgc	atg	tcg	gcg	cag	gtc	ggc	gag	ggt	tcg	1679	
Asn	Arg	Ala	Val	Gly	Asp	Arg	Met	Ser	Ala	Gln	Val	Gly	Glu	Gly	Ser		
				390					395					400			
ctc	gcc	gcc	gcg	gcg	gcg	ctc	gtg	ctg	ctc	ggc	ccg	ttc	acc	ccg	atg	1727	
Leu	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Val	Leu	Gly	Pro	Phe	Thr	Pro	Met		
			405					410					415				
ctg	ttc	atg	ggc	gag	gag	tgg	ggc	gcg	cgc	acc	ccg	tgg	cag	ttc	ttc	1775	
Leu	Phe	Met	Gly	Glu	Glu	Trp	Gly	Ala	Arg	Thr	Pro	Trp	Gln	Phe	Phe		
		420					425					430					

acc tcc cac ccc gag ccc gag ctg ggg gag gcg acg gcg cgc ggg cgc	1823
Thr Ser His Pro Glu Pro Glu Leu Gly Glu Ala Thr Ala Arg Gly Arg	
435 440 445	
atc gcc gag ttc gcc cgc atg ggc tgg gac ccg gca gtc gtg ccc gac	1871
Ile Ala Glu Phe Ala Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp	
450 455 460 465	
ccg cag gac ccg gcc acc ttc gcc cgc tcg cac ctg gac tgg tcc gag	1919
Pro Gln Asp Pro Ala Thr Phe Ala Arg Ser His Leu Asp Trp Ser Glu	
470 475 480	
ccc gag cgg gaa ccg cac gcg ggc ctg ctc gcc ttc tac acc gac ctg	1967
Pro Glu Arg Glu Pro His Ala Gly Leu Leu Ala Phe Tyr Thr Asp Leu	
485 490 495	
atc gcg ctg cgg cgc gag ctg ccg gtc gat gcg ccg gcg cgc gag gtg	2015
Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val	
500 505 510	
gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg	2063
Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu	
515 520 525	
cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggg gtg ccc gag cac	2111
Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His	
530 535 540 545	
ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gcc gga	2159
Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly	
550 555 560	
ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag	2201
Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu	
565 570 575	
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<210> 33
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC

<400> 33
 atgaaccgac gattcccggt ctggg 25

<210> 34
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<220>
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<400> 34
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<210> 35
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<220>
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aaatctagat gaaccgacga ttcccggtct ggcgcg 36

<210> 36
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aaaactagtt tatcactcga ggcgacgat cgcggc 36

<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
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<400> 37
atcgtcgggt catatTTTTT cctcctga 28

<210> 38
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<212> DNA
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<400> 38
aatcaggagg aaaaaatatg aaccgacg 28

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<400> 39
agtggttgt agacgacgtc ct 22

C1
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